

P. Barker
new.
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RAW SEQUENCE LISTING

DATE: 09/20/2002

PATENT APPLICATION: US/09/833,017B

TIME: 13:41:12

Input Set : A:\EP.txt

Output Set: N:\CRF3\09202002\I833017B.raw

3 <110> APPLICANT: CVITKOVITCH, Dennis
5 <120> TITLE OF INVENTION: SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR
TREATMENT OF
6 CRIES
8 <130> FILE REFERENCE: 1889/00401
10 <140> CURRENT APPLICATION NUMBER: 09/833,017B
11 <141> CURRENT FILING DATE: 2001-04-10
13 <160> NUMBER OF SEQ ID NOS: 30
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 141
19 <212> TYPE: DNA
20 <213> ORGANISM: Streptococcus mutans
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23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(141)
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29 1 5 10 15
31 gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96
32 Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
33 20 25 30
35 ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141
36 Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
37 35 40 45
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 46
42 <212> TYPE: PRT
43 <213> ORGANISM: Streptococcus mutans
45 <400> SEQUENCE: 2
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48 1 5 10 15
51 Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
52 20 25 30
55 Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
56 35 40 45
59 <210> SEQ ID NO: 3
60 <211> LENGTH: 63
61 <212> TYPE: DNA
62 <213> ORGANISM: Streptococcus mutans
64 <220> FEATURE:
65 <221> NAME/KEY: CDS
66 <222> LOCATION: (1)..(63)

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70 Ser Gly Ser Leu Ser Thr Phe Phe Arg Leu Phe Asn Arg Ser Phe Thr
71 1          5          10          15
73 caa gct ttg gga aaa .      63
74 Gln Ala Leu Gly Lys
75          20
78 <210> SEQ ID NO: 4
79 <211> LENGTH: 21
80 <212> TYPE: PRT
81 <213> ORGANISM: Streptococcus mutans
83 <400> SEQUENCE: 4
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86 1          5          10          15
89 Gln Ala Leu Gly Lys
90          20
93 <210> SEQ ID NO: 5
94 <211> LENGTH: 1326
95 <212> TYPE: DNA
96 <213> ORGANISM: Streptococcus mutans
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (1)..(1326)
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104 Met Asn Glu Ala Leu Met Ile Leu Ser Asn Gly Leu Leu Thr Tyr Leu
105 1          5          10          15
107 acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act      96
108 Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
109          20          25          30
111 tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata      144
112 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
113          35          40          45
115 atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag      192
116 Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
117          50          55          60
119 cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt      240
120 Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
121 65          70          75          80
123 ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac      288
124 Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
125          85          90          95
127 ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga      336
128 Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
129          100          105          110
131 att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca      384
132 Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
133          115          120          125
135 gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att      432

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136	Gly	Ile	Ala	Leu	Ser	Tyr	Leu	Phe	Leu	Ser	Val	Phe	Asn	Val	Asp	Ile	
137		130					135					140					
139	ggt	cga	ctt	aaa	gat	agt	ttg	acc	aag	atg	aag	gtc	aaa	aaa	cgc	ttg	480
140	Gly	Arg	Leu	Lys	Asp	Ser	Leu	Thr	Lys	Met	Lys	Val	Lys	Lys	Arg	Leu	
141	145						150					155				160	
143	att	cca	atg	aat	att	act	atg	ctt	cta	tac	tac	ctt	tta	ata	cag	gta	528
144	Ile	Pro	Met	Asn	Ile	Thr	Met	Leu	Leu	Tyr	Tyr	Leu	Leu	Ile	Gln	Val	
145							165					170				175	
147	ttg	tat	gtt	ata	gag	agt	tat	aat	gtg	ata	cgc	act	tta	aaa	ttt	cgt	576
148	Leu	Tyr	Val	Ile	Glu	Ser	Tyr	Asn	Val	Ile	Pro	Thr	Leu	Lys	Phe	Arg	
149							180									190	
151	aaa	ttt	gtc	gtt	att	gtc	tat	ctt	att	tta	ttt	ttg	att	ctg	atc	tca	624
152	Lys	Phe	Val	Val	Ile	Val	Tyr	Leu	Ile	Leu	Phe	Leu	Ile	Leu	Ile	Ser	
153							195									205	
155	ttt	tta	agc	caa	tat	acc	aaa	caa	aag	gtt	caa	aat	gag	ata	atg	gca	672
156	Phe	Leu	Ser	Gln	Tyr	Thr	Lys	Gln	Lys	Val	Gln	Asn	Glu	Ile	Met	Ala	
157		210					215									220	
159	caa	aag	gaa	gct	cag	att	cga	aat	atc	acc	cag	tat	agt	cag	caa	ata	720
160	Gln	Lys	Glu	Ala	Gln	Ile	Arg	Asn	Ile	Thr	Gln	Tyr	Ser	Gln	Gln	Ile	
161	225						230									240	
163	gaa	tct	ctt	tac	aag	gat	att	cga	agt	ttc	cgc	cat	gat	tat	ctg	aat	768
164	Glu	Ser	Leu	Tyr	Lys	Asp	Ile	Arg	Ser	Phe	Arg	His	Asp	Tyr	Leu	Asn	
165							245									255	
167	att	tta	act	agc	ctc	aga	tta	ggc	att	gaa	aat	aaa	gat	tta	gct	agt	816
168	Ile	Leu	Thr	Ser	Leu	Arg	Leu	Gly	Ile	Glu	Asn	Lys	Asp	Leu	Ala	Ser	
169							260									270	
171	att	gaa	aag	att	tac	cat	caa	atc	tta	gaa	aaa	aca	gga	cat	caa	ttg	864
172	Ile	Glu	Lys	Ile	Tyr	His	Gln	Ile	Leu	Glu	Lys	Thr	Gly	His	Gln	Leu	
173							275									285	
175	cag	gat	acc	cgt	tat	aat	atc	ggc	cat	cta	gct	aat	att	caa	aac	gat	912
176	Gln	Asp	Thr	Arg	Tyr	Asn	Ile	Gly	His	Leu	Ala	Asn	Ile	Gln	Asn	Asp	
177		290					295									300	
179	gct	gtc	aag	ggt	atc	ttg	tca	gca	aaa	atc	tta	gaa	gct	cag	aat	aaa	960
180	Ala	Val	Lys	Gly	Ile	Leu	Ser	Ala	Lys	Ile	Leu	Glu	Ala	Gln	Asn	Lys	
181	305						310									320	
183	aag	att	gct	gtc	aat	gta	gaa	gtc	tca	agt	aaa	ata	caa	ctg	cct	gag	1008
184	Lys	Ile	Ala	Val	Asn	Val	Glu	Val	Ser	Ser	Lys	Ile	Gln	Leu	Pro	Glu	
185							325									335	
187	atg	gag	ttg	ctt	gat	ttc	att	acc	ata	ctt	tct	atc	ttg	tgt	gat	aat	1056
188	Met	Glu	Leu	Leu	Asp	Phe	Ile	Thr	Ile	Leu	Ser	Ile	Leu	Cys	Asp	Asn	
189							340									350	
191	gcc	att	gag	gct	gct	ttc	gaa	tca	tta	aat	cct	gaa	att	cag	tta	gcc	1104
192	Ala	Ile	Glu	Ala	Ala	Phe	Glu	Ser	Leu	Asn	Pro	Glu	Ile	Gln	Leu	Ala	
193							355									365	
195	ttt	ttt	aag	aaa	aat	ggc	agt	ata	gtc	ttt	atc	att	cag	aat	tcc	acc	1152
196	Phe	Phe	Lys	Lys	Asn	Gly	Ser	Ile	Val	Phe	Ile	Ile	Gln	Asn	Ser	Thr	
197		370					375									380	
199	aaa	gaa	aaa	caa	ata	gat	gtg	agt	aaa	att	ttt	aaa	gaa	aac	tat	tcc	1200
200	Lys	Glu	Lys	Gln	Ile	Asp	Val	Ser	Lys	Ile	Phe	Lys	Glu	Asn	Tyr	Ser	

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201 385          390          395          400
203 act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att      1248
204 Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
205          405          410          415
207 ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat      1296
208 Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
209          420          425          430
211 tta ttc aag caa ctc cta ata ata aaa tag      1326
212 Leu Phe Lys Gln Leu Leu Ile Ile Lys
213          435          440
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 441
218 <212> TYPE: PRT
219 <213> ORGANISM: Streptococcus mutans
221 <400> SEQUENCE: 6
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227 Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
228          20          25          30
231 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
232          35          40          45
235 Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
236          50          55          60
239 Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
240 65          70          75          80
243 Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
244          85          90          95
247 Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
248          100          105          110
251 Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
252          115          120          125
255 Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
256          130          135          140
259 Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
260 145          150          155          160
263 Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
264          165          170          175
267 Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
268          180          185          190
271 Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
272          195          200          205
275 Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
276          210          215          220
279 Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
280 225          230          235          240
283 Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
284          245          250          255
287 Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
288          260          265          270

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291 Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
292           275           280           285
295 Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
296           290           295           300
299 Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
300 305           310           315           320
303 Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
304           325           330           335
307 Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
308           340           345           350
311 Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
312           355           360           365
315 Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
316           370           375           380
319 Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
320 385           390           395           400
323 Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
324           405           410           415
327 Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
328           420           425           430
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332           435           440
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336 <211> LENGTH: 750
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338 <213> ORGANISM: Streptococcus mutans
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342 <222> LOCATION: (1)..(750)
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347 1           5           10           15
349 ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat      96
350 Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
351           20           25           30
353 aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc      144
354 Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
355           35           40           45
357 cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa      192
358 Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
359           50           55           60
361 aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat      240
362 Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
363 65           70           75           80
365 aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg      288
366 Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
367           85           90           95
369 ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa      336

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VERIFICATION SUMMARY

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Input Set : A:\EP.txt

Output Set: N:\CRF3\09202002\I833017B.raw

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L:657 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:670 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:683 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
- L:696 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
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